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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/658,745

DATE: 09/29/2003

TIME: 15:05:10

Input Set : N:\Crf3\RULE60\10658745.txt

Output Set: N:\CRF4\09292003\J658745.raw

ENTERED

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3 <110> APPLICANT: Biogen, Inc.
4     Burkly, Linda
5     Wang, Li Chun
7 <120> TITLE OF INVENTION: METHODS OF MODULATING LIPID METABOLISM AND STORAGE
9 <130> FILE REFERENCE: A069PCT
11 <140> CURRENT APPLICATION NUMBER: 10/658,745
12 <141> CURRENT FILING DATE: 2003-09-08
15 <150> PRIOR APPLICATION NUMBER: 09/704,917
16 <151> PRIOR FILING DATE: 2000-11-02
18 <150> PRIOR APPLICATION NUMBER: PCT/US00/05662
19 <151> PRIOR FILING DATE: 2000-03-03
22 <150> PRIOR APPLICATION NUMBER: 60/122,640
23 <151> PRIOR FILING DATE: 1999-03-03
25 <150> PRIOR APPLICATION NUMBER: 60/124,446
26 <151> PRIOR FILING DATE: 1999-03-15
28 <160> NUMBER OF SEQ ID NOS: 22
30 <170> SOFTWARE: PatentIn Ver. 2.1
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 1277
34 <212> TYPE: DNA
35 <213> ORGANISM: Gallus sp.
37 <220> FEATURE:
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (1)..(1275)
41 <400> SEQUENCE: 1
42 atg gtc gaa atg ctg ctg ttg aca aga att ctc ttg gtg ggc ttc atc      48
43 Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
44   1               5               10               15
46 tgc gct ctt tta gtc tcc tct ggg ctg act tgt gga cca ggc agg ggc      96
47 Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
48   20               25               30
50 att gga aaa agg agg cac ccc aaa aag ctg acc ccg tta gcc tat aag      144
51 Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
52   35               40               45
54 cag ttt att ccc aat gtg gca gag aag acc cta ggg gcc agt gga aga      192
55 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
56   50               55               60
58 tat gaa ggg aag atc aca aga aac tcc gag aga ttt aaa gaa cta acc      240
59 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
60  65               70               75               80
62 cca aat tac aac cct gac att att ttt aag gat gaa gag aac acg gga      288
63 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
64   85               90               95

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66 gct gac aga ctg atg act cag cgc tgc aag gac aag ctg aat gcc ctg 336
67 Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
68 100 105 110
70 gcg atc tcg gtg atg aac cag tgg ccc ggg gtg aag ctg cgg gtg acc 384
71 Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
72 115 120 125
74 gag ggc tgg gac gag gat ggc cat cac tcc gag gaa tcg ctg cac tac 432
75 Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
76 130 135 140
78 gag ggt cgc gcc gtg gac atc acc acg tcg gat cgg gac cgc agc aag 480
79 Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys
80 145 150 155 160
82 tac gga atg ctg gcc cgc ctc gcc gtc gag gcc ggc ttc gac tgg gtc 528
83 Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
84 165 170 175
86 tac tac gag tcc aag gcg cac atc cac tgc tcc gtc aaa gca gaa aac 576
87 Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
88 180 185 190
90 tca gtg gca gcg aaa tca gga ggc tgc ttc cct ggc tca gcc aca gtg 624
91 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
92 195 200 205
94 cac ctg gag cat gga ggc acc aag ctg gtg aag gac ctg agc cct ggg 672
95 His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
96 210 215 220
98 gac cgc gtg ctg gct gct gac gcg gac ggc cgg ctg ctc tac agt gac 720
99 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
100 225 230 235 240
102 ttc ctc acc ttc ctc gac cgg atg gac agc tcc cga aag ctc ttc tac 768
103 Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
104 245 250 255
106 gtc atc gag acg cgg cag ccc cgg gcc cgg ctg cta ctg acg gcg gcc 816
107 Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala
108 260 265 270
110 cac ctg ctc ttt gtg gcc ccc cag cac aac cag tcg gag gcc aca ggg 864
111 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
112 275 280 285
114 tcc acc agt ggc cag gcg ctc ttc gcc agc aac gtg aag cct ggc caa 912
115 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
116 290 295 300
118 cgt gtc tat gtg ctg ggc gag ggc ggg cag cag ctg ctg ccg gcg tct 960
119 Arg Val Tyr Val Leu Gly Glu Gly Gln Gln Leu Leu Pro Ala Ser
120 305 310 315 320
122 gtc cac agc gtc tca ttg cgg gag gag gcg tcc gga gcc tac gcc cca 1008
123 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
124 325 330 335
126 ctc acc gcc cag ggc acc atc ctc atc aac cgg gtg ttg gcc tcc tgc 1056
127 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
128 340 345 350
130 tac gcc gtc atc gag gag cac agt tgg gcc cat tgg gcc ttc gca cca 1104

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Input Set : N:\CrF3\RULE60\10658745.txt

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131 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
132      355      360      365
134 ttc cgc ttg gct cag ggg ctg ctg gcc gcc ctc tgc cca gat ggg gcc 1152
135 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
136      370      375      380
138 atc cct act gcc gcc acc acc acc act ggc atc cat tgg tac tca cgg 1200
139 Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
140 385      390      395      400
142 ctc ctc tac cgc atc ggc agc tgg gtg ctg gat ggt gac gcg ctg cat 1248
143 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
144      405      410      415
146 ccg ctg ggc atg gtg gca ccg gcc agc tg 1277
147 Pro Leu Gly Met Val Ala Pro Ala Ser
148      420      425
150 <210> SEQ ID NO: 2
151 <211> LENGTH: 1190
152 <212> TYPE: DNA
153 <213> ORGANISM: Murine sp.
155 <220> FEATURE:
156 <221> NAME/KEY: CDS
157 <222> LOCATION: (1)..(1188)
159 <400> SEQUENCE: 2
160 atg gct ctg ccg gcc agt ctg ttg ccc ctg tgc tgc ttg gca ctc ttg 48
161 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
162 1 5 10 15
164 gca cta tct gcc cag agc tgc ggg ccg ggc cga gga ccg gtt ggc cgg 96
165 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
166 20 25 30
168 cgg cgt tat gtg cgc aag caa ctt gtg cct ctg cta tac aag cag ttt 144
169 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
170 35 40 45
172 gtg ccc agt atg ccc gag cgg acc ctg ggc gcg agt ggg cca gcg gag 192
173 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
174 50 55 60
176 ggg agg gta aca agg ggg tcg gag cgc ttc cgg gac ctc gta ccc aac 240
177 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
178 65 70 75 80
180 tac aac ccc gac ata atc ttc aag gat gag gag aac agc ggc gca gac 288
181 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
182 85 90 95
184 cgc ctg atg aca gag cgt tgc aaa gag cgg gtg aac gct cta gcc atc 336
185 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
186 100 105 110
188 gcg gtg atg aac atg tgg ccc gga gta cgc cta cgt gtg act gaa ggc 384
189 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
190 115 120 125
192 tgg gac gag gac ggc cac cac gca cag gat tca ctc cac tac gaa ggc 432
193 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
194 130 135 140

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Input Set : N:\Crf3\RULE60\10658745.txt

Output Set: N:\CRF4\09292003\J658745.raw

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196 cgt gcc ttg gac atc acc acg tct gac cgt gac cgt aat aag tat ggt 480
197 Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
198 145 150 155 160
200 ttg ttg gcg cgc cta gct gtg gaa gcc gga ttc gac tgg gtc tac tac 528
201 Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
202 165 170 175
204 gag tcc cgc aac cac atc cac gta tcg gtc aaa gct gat aac tca ctg 576
205 Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
206 180 185 190
208 gcg gtc cga gcc gga ggc tgc ttt ccg gga aat gcc acg gtg cgc ttg 624
209 Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
210 195 200 205
212 cgg agc ggc gaa cgg aag ggg ctg agg gaa cta cat cgt ggt gac tgg 672
213 Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
214 210 215 220
216 gta ctg gcc gct gat gca gcg ggc cga gtg gta ccc acg cca gtg ctg 720
217 Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu
218 225 230 235 240
220 ctc ttc ctg gac cgg gat ctg cag cgc cgc gcc tcg ttc gtg gct gtg 768
221 Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
222 245 250 255
224 gag acc gag cgg cct ccg cgc aaa ctg ttg ctc aca ccc tgg cat ctg 816
225 Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
226 260 265 270
228 gtg ttc gct gct cgc ggg cca gcg cct gct cca ggt gac ttt gca ccg 864
229 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
230 275 280 285
232 gtg ttc gcg cgc cgc tta cgt gct ggc gac tcg gtg ctg gct ccc ggc 912
233 Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
234 290 295 300
236 ggg gac gcg ctc cag ccg gcg cgc gta gcc cgc gtg gcg cgc gag gaa 960
237 Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
238 305 310 315 320
240 gcc gtg ggc gtg ttc gca ccg ctc act gcg cac ggg acg ctg ctg gtc 1008
241 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
242 325 330 335
244 aac gac gtc ctc gcc tcc tgc tac gcg gtt cta gag agt cac cag tgg 1056
245 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
246 340 345 350
248 gcc cac cgc gcc ttc gcc cct ttg cgg ctg ctg cac gcg ctc ggg gct 1104
249 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
250 355 360 365
252 ctg ctc cct ggg ggt gca gtc cag ccg act ggc atg cat tgg tac tct 1152
253 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
254 370 375 380
256 cgc ctc ctt tac cgc ttg gcc gag gag tta atg ggc tg 1190
257 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
258 385 390 395
260 <210> SEQ ID NO: 3

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Input Set : N:\Crf3\RULE60\10658745.txt

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261 <211> LENGTH: 1281
262 <212> TYPE: DNA
263 <213> ORGANISM: Murine sp.
265 <220> FEATURE:
266 <221> NAME/KEY: CDS
267 <222> LOCATION: (1)..(1233)
269 <400> SEQUENCE: 3
270 atg tct ccc gcc tgg ctc cgg ccc cga ctg cgg ttc tgt ctg ttc ctg 48
271 Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
272 1 5 10 15
274 ctg ctg ctg ctt ctg gtg ccg gcg gcg cgg ggc tgc ggg ccg ggc cgg 96
275 Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
276 20 25 30
278 gtg gtg ggc agc cgc cgg agg ccg cct cgc aag ctc gtg cct ctt gcc 144
279 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
280 35 40 45
282 tac aag cag ttc agc ccc aac gtg ccg gag aag acc ctg ggc gcc agc 192
283 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
284 50 55 60
286 ggg cgc tac gaa ggc aag atc gcg cgc agc tct gag cgc ttc aaa gag 240
287 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
288 65 70 75 80
290 ctc acc ccc aac tac aat ccc gac atc atc ttc aag gac gag gag aac 288
291 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
292 85 90 95
294 acg ggt gcc gac cgc ctc atg acc cag cgc tgc aag gac cgt ctg aac 336
295 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
296 100 105 110
298 tca ctg gcc atc tct gtc atg aac cag tgg cct ggt gtg aaa ctg cgg 384
299 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
300 115 120 125
302 gtg acc gaa ggc cgg gat gaa gat ggc cat cac tca gag gag tct tta 432
303 Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
304 130 135 140
306 cac tat gag ggc cgc gcg gtg gat atc acc acc tca gac cgt gac cga 480
307 His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
308 145 150 155 160
310 aat aag tat gga ctg ctg gcg cgc tta gca gtg gag gcc ggc ttc gac 528
311 Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
312 165 170 175
314 tgg gtg tat tac gag tcc aag gcc cac gtg cat tgc tct gtc aag tct 576
315 Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
316 180 185 190
318 gag cat tcg gcc gct gcc aag aca ggt ggc tgc ttt cct gcc gga gcc 624
319 Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
320 195 200 205
322 cag gtg cgc cta gag aac ggg gag cgt gtg gcc ctg tca gct gta aag 672
323 Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys
324 210 215 220

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/658,745

DATE: 09/29/2003
TIME: 15:05:11

Input Set : N:\Crf3\RULE60\10658745.txt
Output Set: N:\CRF4\09292003\J658745.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; N Pos. 1387,1388,1389

Seq#:6; Xaa Pos. 463

Seq#:15; Xaa Pos. 463

Seq#:21; Xaa Pos. 7,9,44,85,93,98,112,132,137,139,181,183,185,186,189,191

Seq#:21; Xaa Pos. 196,200,206,207,209,211,212,216,217,219

Seq#:22; Xaa Pos. 7,8,9,12,13,14,17,19,22,27,29,30,31,33,40,41,44,45,46,48

Seq#:22; Xaa Pos. 53,54,71,79,83,84,85,87,95,100,107,114,115,116,125,134

Seq#:22; Xaa Pos. 135,139,141,157,158,160,162,166,167

VARIABLE LOCATION SUMMARY

DATE: 09/29/2003

PATENT APPLICATION: US/10/658,745

TIME: 15:05:11

Input Set : N:\Crf3\RULE60\10658745.txt

Output Set: N:\CRF4\09292003\J658745.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:6; N Pos. 1387,1388,1389

Seq#:6; Xaa Pos. 463

Seq#:15; Xaa Pos. 463

Seq#:21; Xaa Pos. 7,9,44,85,93,98,112,132,137,139,181,183,185,186,189,191

Seq#:21; Xaa Pos. 196,200,206,207,209,211,212,216,217,219

Seq#:22; Xaa Pos. 7,8,9,12,13,14,17,19,22,27,29,30,31,33,40,41,44,45,46,48

Seq#:22; Xaa Pos. 53,54,71,79,83,84,85,87,95,100,107,114,115,116,125,134

Seq#:22; Xaa Pos. 135,139,141,157,158,160,162,166,167

VERIFICATION SUMMARY

DATE: 09/29/2003

PATENT APPLICATION: US/10/658,745

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Input Set : N:\Crf3\RULE60\10658745.txt

Output Set: N:\CRF4\09292003\J658745.raw

L:742 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:1344
M:341 Repeated in SeqNo=6
L:1627 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:15
L:1627 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:15
L:1627 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:448
L:2228 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:21
L:2228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
M:341 Repeated in SeqNo=21
L:2461 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:22
L:2461 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
M:341 Repeated in SeqNo=22